

## SEQUENCE LISTING

&lt;120&gt; METHODS OF DIAGNOSING NEUROPSYCHIATRIC DISORDERS

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<140> 09/722,544

<141> 2000-11-28

<150> 09/236,134

<151> 1999-01-22

<150> 60/078,044

<151> 1998-03-16

<150> 60/088,312

<151> 1998-06-05

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<151> 1998-10-28

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gttcttagct	cactgaagcc	tcaaattcct	gggttcaagt	gaccctccca	cctcagcccc	240
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gga gat att gca aat aac agc ggg aac atg aag ccg cca ctc ttg gtg 392  
Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro Pro Leu Leu Val  
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Phe	Ile	Val	Cys	Leu	Leu	Trp	Leu	Lys	Asp	Ser	His	Cys	Ala	Pro	Thr	
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Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe Ser Glu	
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gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg act ggt	536
Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu Thr Gly	
70 75 80	
att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa cac acc	584
Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu His Thr	
85 90 95 100	
aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag gag gcc	632
Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln Glu Ala	
105 110 115	
ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa gaa agg	680
Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu Glu Arg	
120 125 130	
cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg tct tgc	728
Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys	
135 140 145	
ctg gaa aat aac tgc atg aga att tat aca acc tgc caa cct agc tgg	776
Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro Ser Trp	
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Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile Tyr Gln	
165 170 175 180	
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Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp Leu Pro Ile Ser	
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200 205 210	
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Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe Asn Arg Ser Phe	
215 220 225	
aac gtc ttc aga cag atg cag caa gag ttt gac cag act ttt caa tca	1016
Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe Gln Ser	
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cat ttc ata tca gat aca gac cta act gag cct tac ttt ttt cca gct	1064
His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr Phe Phe Pro Ala	
245 250 255 260	
ttc tct aaa gag ccg atg aca aaa gca gat ctt gag caa tgt tgg gac	1112
Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu Gln Cys Trp Asp	
265 270 275	

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Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val Ser Ile Tyr	
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Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys Ala Ile Glu Asp	
295 300 305	
tta cca aaa caa gac aaa gct cct gac cac gga ggc ctg att tca aag	1256
Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly Leu Ile Ser Lys	
310 315 320	
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Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu Asp Gln Asn	
325 330 335 340	
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Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys Cys Gln Ala	
345 350 355	
cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca gaa tta	1400
His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr Glu Leu	
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gac gag gcg atc agg ttg gtc aat gta tcc aat cag cag tat ggc cag	1448
Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr Gly Gln	
375 380 385	
att ctc cag atg acc cgg aag cac ttg gag gac acc gcc tat ctg gtg	1496
Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr Leu Val	
390 395 400	
gag aag atg aga ggg caa ttt ggc tgg gtg tct gaa ctg gca aac cag	1544
Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala Asn Gln	
405 410 415 420	
gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt cca agg	1592
Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val Pro Arg	
425 430 435	
att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg aca gac	1640
Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met Thr Asp	
440 445 450	
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Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro Leu Glu	
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gaa agt gct gag agt tct aac ttc att ggc tac gta gtg gca aaa gct	1736
Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val Ala Lys Ala	
470 475 480	
cta cag cat ttt aag gaa cat ttt aaa acc tgg taagaagatc taatgcatcc	1789
Leu Gln His Phe Lys Glu His Phe Lys Thr Trp	
485 490 495	
tatatccagt aagtagaatt atctcttcat ctgggacctg gaaatcctga aataaaaaag	1849

gataatgcaa taaacacagt tgcaggaaag tatgttagct atatactatg aagtactctt 1909  
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 Cys Ala Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys  
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 Ser Phe Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys  
 65 70 75 80  
 Ala Leu Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu  
 85 90 95  
 Lys Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu  
 100 105 110  
 Lys Gln Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu  
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 Glu Glu Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu  
 130 135 140  
 Cys Arg Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys  
 145 150 155 160  
 Gln Pro Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg  
 165 170 175  
 Lys Ile Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp  
 180 185 190  
 Leu Pro Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln  
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 Met Glu Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe  
 210 215 220  
 Asn Arg Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln  
 225 230 235 240  
 Thr Phe Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr  
 245 250 255  
 Phe Phe Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu  
 260 265 270  
 Gln Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser  
 275 280 285  
 Val Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys  
 290 295 300  
 Ala Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly  
 305 310 315 320  
 Leu Ile Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu  
 325 330 335  
 Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln  
 340 345 350  
 Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu  
 355 360 365

His Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln  
 370 375 380  
 Gln Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr  
 385 390 395 400  
 Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu  
 405 410 415  
 Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln  
 420 425 430  
 Val Val Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr  
 435 440 445  
 Met Met Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys  
 450 455 460  
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 gttcwttagct cactgaagcc tcaaattcct gggttcaagt gaccctccya cctcagcccc 240  
 atg agg acc tgg gac tac agt aac agc ggg aac atg aag ccg cca ctc 288  
 Met Arg Thr Trp Asp Tyr Ser Asn Ser Gly Asn Met Lys Pro Pro Leu  
 1 5 10 15  
  
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 ccc act tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt 384  
 Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe  
 35 40 45  
  
 tct gag gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg 432  
 Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu  
 50 55 60  
  
 act ggt att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa 480  
 Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu  
 65 70 75 80  
  
 cac acc aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag 528  
 His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln  
 85 90 95  
  
 gag gcc ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa 576  
 Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu

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agc tgg tcc tct gtg aaa aat aag att gaa cgg ttt ttc agg aag ata Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile 145 150 155 160			720
tat caa ttt cta ttt cct ttc cat gaa gat aat gaa aaa gat ctc ccc Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp Leu Pro 165 170 175			768
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agt ttt aac gtc ttc aga cag atg cag caa gag ttt gac cag act ttt Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe 210 215 220			912
caa tca cat ttc ata tca gat aca gac cta act gag cct tac ttt ttt Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr Phe Phe 225 230 235 240			960
cca gct ttc tct aaa gag ccg atg aca aaa gca gat ctt gag caa tgt Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu Gln Cys 245 250 255			1008
tgg gac att ccc aac ttc ttc cag ctg ttt tgt aat ttc agt gtc tct Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val Ser 260 265 270			1056
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tca aag atg tta cct ggg cag gac aga gga ctg tgt ggg gaa ctt gac Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu Asp 305 310 315 320			1200
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 Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr  
 370 375 380  
 ctg gtg gag aag atg aga ggg caa ttt ggc tgg gtg tct gaa ctg gca 1440  
 Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala  
 385 390 395 400  
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 Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met  
 420 425 430  
 aca gac tta agc att ctg cct tcc tct aat ttc aca ctc aag atc cct 1584  
 Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro  
 435 440 445  
 ctt gaa gaa agt gct gag agt tct aac ttc att ggc tac gta gtg gca 1632  
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 Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp  
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<211> 477

<212> PRT

<213> Homo sapiens

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 Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe  
 35 40 45  
 Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu  
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Thr	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg	Lys	Glu	Lys	Glu	65	70	75	80
His	Thr	Asn	Leu	Met	Ser	Thr	Leu	Lys	Lys	Cys	Arg	Glu	Glu	Lys	Gln	85	90	95	
Glu	Ala	Leu	Lys	Leu	Leu	Asn	Glu	Val	Gln	Glu	His	Leu	Glu	Glu	Glu	100	105	110	
Glu	Arg	Leu	Cys	Arg	Glu	Ser	Leu	Ala	Asp	Ser	Trp	Gly	Glu	Cys	Arg	115	120	125	
Ser	Cys	Leu	Glu	Asn	Asn	Cys	Met	Arg	Ile	Tyr	Thr	Thr	Cys	Gln	Pro	130	135	140	
Ser	Trp	Ser	Ser	Val	Lys	Asn	Lys	Ile	Glu	Arg	Phe	Phe	Arg	Lys	Ile	145	150	155	160
Tyr	Gln	Phe	Leu	Phe	Pro	Phe	His	Glu	Asp	Asn	Glu	Lys	Asp	Leu	Pro	165	170	175	
Ile	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Asp	Ala	Gln	Leu	Thr	Gln	Met	Glu	180	185	190	
Asp	Val	Phe	Ser	Gln	Leu	Thr	Val	Asp	Val	Asn	Ser	Leu	Phe	Asn	Arg	195	200	205	
Ser	Phe	Asn	Val	Phe	Arg	Gln	Met	Gln	Gln	Glu	Phe	Asp	Gln	Thr	Phe	210	215	220	
Gln	Ser	His	Phe	Ile	Ser	Asp	Thr	Asp	Leu	Thr	Glu	Pro	Tyr	Phe	Phe	225	230	235	240
Pro	Ala	Phe	Ser	Lys	Glu	Pro	Met	Thr	Lys	Ala	Asp	Leu	Glu	Gln	Cys	245	250	255	
Trp	Asp	Ile	Pro	Asn	Phe	Phe	Gln	Leu	Phe	Cys	Asn	Phe	Ser	Val	Ser	260	265	270	
Ile	Tyr	Glu	Ser	Val	Ser	Glu	Thr	Ile	Thr	Lys	Met	Leu	Lys	Ala	Ile	275	280	285	
Glu	Asp	Leu	Pro	Lys	Gln	Asp	Lys	Ala	Pro	Asp	His	Gly	Gly	Leu	Ile	290	295	300	
Ser	Lys	Met	Leu	Pro	Gly	Gln	Asp	Arg	Gly	Leu	Cys	Gly	Glu	Leu	Asp	305	310	315	320
Gln	Asn	Leu	Ser	Arg	Cys	Phe	Lys	Phe	His	Glu	Lys	Cys	Gln	Lys	Cys	325	330	335	
Gln	Ala	His	Leu	Ser	Glu	Asp	Cys	Pro	Asp	Val	Pro	Ala	Leu	His	Thr	340	345	350	
Glu	Leu	Asp	Glu	Ala	Ile	Arg	Leu	Val	Asn	Val	Ser	Asn	Gln	Gln	Tyr	355	360	365	
Gly	Gln	Ile	Leu	Gln	Met	Thr	Arg	Lys	His	Leu	Glu	Asp	Thr	Ala	Tyr	370	375	380	
Leu	Val	Glu	Lys	Met	Arg	Gly	Gln	Phe	Gly	Trp	Val	Ser	Glu	Leu	Ala	385	390	395	400
Asn	Gln	Ala	Pro	Glu	Thr	Glu	Ile	Ile	Phe	Asn	Ser	Ile	Gln	Val	Val	405	410	415	
Pro	Arg	Ile	His	Glu	Gly	Asn	Ile	Ser	Lys	Gln	Asp	Glu	Thr	Met	Met	420	425	430	
Thr	Asp	Leu	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Leu	Lys	Ile	Pro	435	440	445	
Leu	Glu	Glu	Ser	Ala	Glu	Ser	Ser	Asn	Phe	Ile	Gly	Tyr	Val	Val	Ala	450	455	460	
Lys	Ala	Leu	Gln	His	Phe	Lys	Glu	His	Phe	Lys	Thr	Trp				465	470	475	

&lt;210&gt; 5

&lt;211&gt; 1485

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 5

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